

Applicant: Rajasekhar Bandaru
Title: 68730 and 69112, Protein Kinase Molecules and Uses
Therefor
Attorney/Agent: Jill Uhl
Docket No.: MPI2000-521P1R(M)

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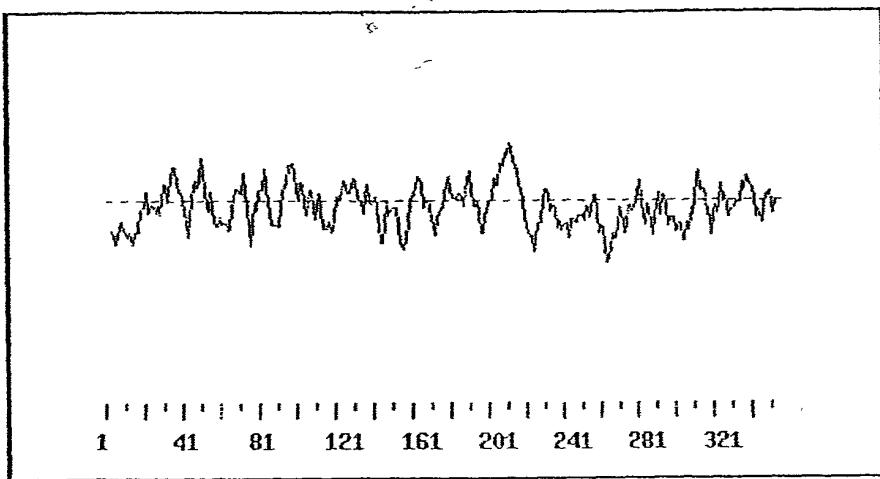


FIGURE 1

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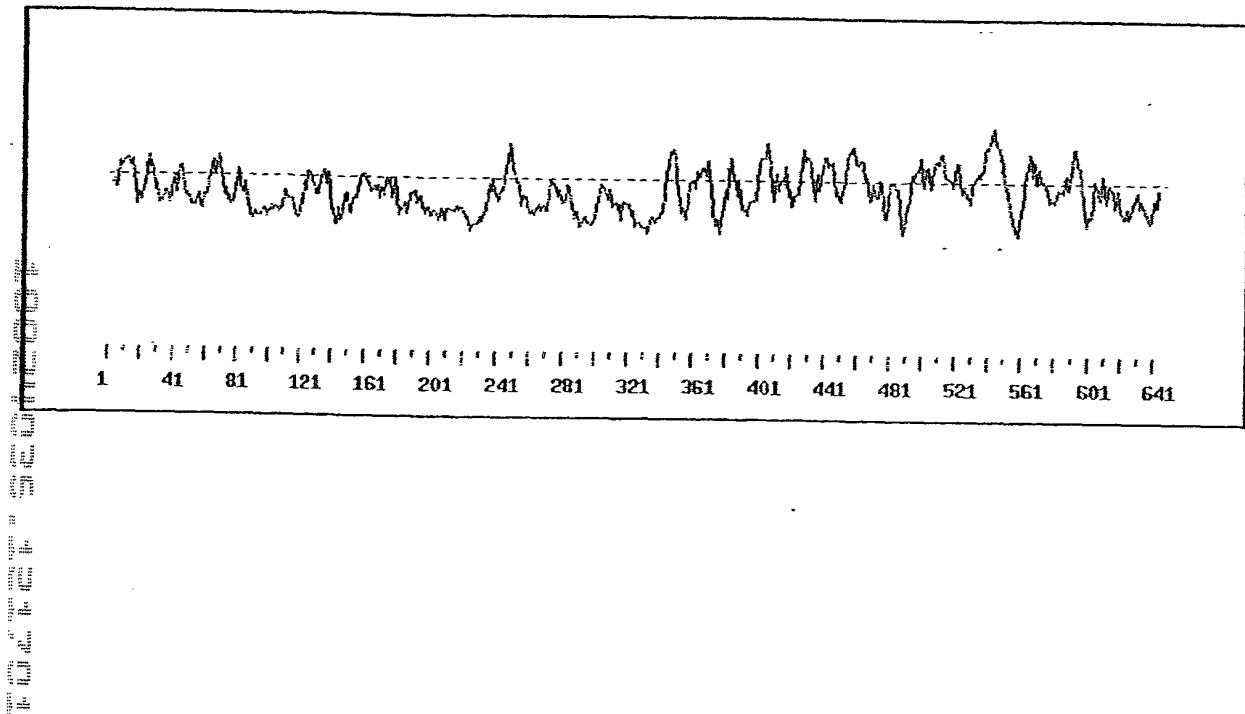


FIGURE 2

pkinase: domain 1 of 1, from 23 to 279: score 346.3, E = 3.4e-100
 *->yelleklGeGsfGkVykakhk.tgkivAvKilkkesls.....1rE
 +e++e+1G G+f++V +a++k tgk++AvK++k+ 1++++++ +E
 68730 23 FEFKÉTLGTGAFSEVVLAAEKATGKLFAVKCIPKKALKgkessiENE 69

iqilkrlsHpNivrllgvfedtddhlylvmEymegGdLfdylrnnoplse
 i++l++++H+Niv 1 +++e +++hlylvm+++ gG+Lfd+++++g ++e
 68730 70 IAVLRKIKHENIVALEDIYE-SPNHLYLVMQLVSGGELFDRIVEKGFYTE 118

keakkialQilrGleYLHsngivHRDLKpeNILden...gtvKiaDFGL
 k+a +++Q+1 ++ YLH++givHRDLKpeN+L +++++ ++ i+DFGL
 68730 119 KDASTLIROVLDAVYYLHRMGIVHRDDLKPENLLYYSQdeesSKIMISDFGL 168

Ar11...eklttfvGTpwYmmAPEvilegrgysskvDvWS1GviLyEl1t
 ++ +++ +++t +GTp+Y+ APEv 1 +++ys++vD WS+Gvi y ll+
 68730 169 SKMEgkgDVMSTACGTPGYV-APEV-LAQKPYSKAVDCWSIGVIAYILLC 216

ggplfpgadlpaftggdevdql*ii*fvlk1Pfsdelpktridpleelfrik
 g +Pf+d ++ ++lf+ +
 68730 217 G-----YPPFYD-----ENDSKLFEQI 233

kr.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<
 ++ + + +p ++ +S++kd++ + +kDP+kR+ t++++ hpw+
 68730 234 LKaeyefDSPYWDDISDSAKDFIRNLMEKDPNKRY---TCEQAARHPWI 279

-*

FIGURE 3A

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serkin_6: domain 1 of 1, from 23 to 279: score 386.6, E = 2.5e-112
 *->Yellkk1GkGaFGkVylardkktgrlvAiKvik.....erilrE
 +e+ ++1G GaF++V la +k tg+l+A+K+i+++ +++ +i++E
 68730 23 FEFKETLGTGAFSEVLAEEKATGKLFAVKCIPkkalkgkeSSIENE 69

ikilkk.dHPNIVkLydvvfed.dkly1VmEyceGd1GdLfddkkkrgrrg
 i++L+k +H+NIV L d++e+++ly1Vm +++G G+Lfd+++++g
 68730 70 IAVLRKikHENIVALEDIYESpNHLYLVMQLVSG--GELFDRIVEKG-- 115

lrkvlsE.earfyfrQilsaLeYLHsqqIiHRDLKPeNiLLds....hv
 ++E++a ++rQ+l+a+ YLH++gI+HRDLKPeN+L S+++++ +
 68730 116 ---YTEkDASTLIRQVLDAVYYLHRMGIYHRDLKPENLYYSqdeesKI 161

KlaDFG1Arq1.....ttfvGTpeYmAPEv1...gYgkpavDiWS1Gci
 +++DFG1++ +++ +t +GTp Y+APEv1 +++Y+k avD WS+G+i
 68730 162 MISDFGLSKMEdkgdvmSTACGTPGYVAPEVLaqkPYSK-AVDCWSIGVI 210

lyElltGkpPFp..qldlifkkig.....SpeakdLikk1L
 y+1l+G+pPF+++++ +f++i++ +++ ++++++ S++akd+i++l+
 68730 211 AYILLCGYPPFYdeNDSKLFEQILkaeyefdspywddiSDSAKDFIRNLM 260

vkdPekRlta.eaLedaLdikaHPff<-*
 +kdp+kR+t++a + HP++

68730 261 EKDPNKRYTCeQAAR-----HPWI 279

FIGURE 3B

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tyrkin_6: domain 1 of 1, from 23 to 279: score 35.7, E = 4e-14
*->ltlgkkLGeGaFGeVykGt1k...ieVAVKtLkeda...keeFlrE
+++++LG GaF eV++++ k ++ AVK++ + a +++ + +E
68730 23 FEFKETLGTGAFSEVVLAAEKatqKLFAVKCIPKKAlkgkESSIENE 69
akiMkk1GgkHpNiVkLlGvcteegrrFmevePlmivmEymegGdLldyL
+ +++k+ kH+NiV+L + ++ 1++vm ++++gG L d++
68730 70 IAVLRKI--KHENIVALEDIYESP-----NHLYLVMQLVSGGELFDR 110
rknrpklslsdl1sfA1QIAkGMeYLesknfvHRDLAARNcLvgenk...
++ + +d Q+ + YL+++++vHRDL N L+ ++ +++
68730 111 -VEKGFYTEKDASTLIRQVLDAVYYLHRMGIVHRDLKPENLYYSQDees 159
vvKIsDFGLsRdlydddDkkGeskdyYrkkggkggktllPirWmAPEs1kd
+ IsDFGLs+ + + d+ +++ g+ + APE+l
68730 160 KIMISDFGLSKMEGKG-----DVMSTAC--GTPG----YVAPEVLAQ 195
gkFtskSDVWSFGVllWEift1GeqPYpgeiqqfmsneevleylkGyR1
+ ++ + D WS GV + i+ G +P ++ +++ ++e++ k ++
68730 196 KPYSKAVDCWSIGVIAY-ILLCGYPPFYD-----ENDSKLFEQILKAEYE 239
pkPendlpiSs...vtCPdelyd1M1qCWaedPedRPtFsel..verl<
++ ++ + +d + +lM++ dP++R t + + ++ +
68730 240 FDSPY----WddisDSAKDFIRNLMEK---DPNKRYTCEQAarHPWI 279

FIGURE 3C

pkinase: domain 1 of 1, from 356 to 613: score 350.2, E = 2.3e-101
*->yellek1GeGsfGkVykakhk.tgkivAvKilkkesls.....1rE
ye+f++G G+f++V++++h++t + +A+Ki++k++l+++++ +E
69112 356 YETGRVIGDGNFAVVKECRHReTRQAYAMKIIDKSRLKgkedmvDSE 402

iqilkrlsHpNIVrllgvfedtddhlylvmEymegGdLfdy1rrngplse
i i ++lsHpNIV+l++v+e td ++yl++Ey+ gGdLfd + + +++e
69112 403 ILIIQSLSHPNIVKLHEVYE-TDMEIYLILEYVQGGDLFDAIIIESVKFPE 451

keakkialQilrGleYLHsngivHRDLKpeNILLden....gtvKiaDFG
++a ++ ++++++l ++H+++ivHRDLKpeN+L+ +n++++ t+K+aDFG
69112 452 PDAALMIMDLCKALVHMHDKSIVHRDLKPE NLLVQRNedksTTLKLADFG 501

LArl1.eklttfvGTpwYmmAPEvilegrgysskvDvWS1GviLyEl1tg
LA+ + + t++GTp+Y+ APE+ 1+ +gy+ +vD+W+ GviLy 11+g
69112 502 LAKHVVvRPIFTVCGTPTYV-APEI-LSEKGYGLEVDMWAAGVILYILLCG 549

gplfpgadlpafgtggdevdqliifvlklPfsdelpktridpleelfrikk
+Pf+ ++ +elf+ii++
69112 550 -----FPPFRS-----PERDQDELFNIIQ 568

r.....rlplpsncSeelkdL1kkcLnkDPskRpGsatakeilnhpwf<-
++ + ++p ++n+S++kdl++++L +DP+kR+ ta+++l+hpw+
69112 569 LghfefLPPYWDNISDAAKDLVSRLVVDPKKRY---TAHQVLQHPWI 613

FIGURE 4A

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serkin_6: domain 1 of 1, from 356 to 613: score 372.7, E = 3.8e-108
*->Yellkk1GkGaFGkVylardkktgrlvAiKvik.....erilrE
Ye +++++G G F++V+ +r++t + +A+K+i++++ +++++++ +E
69112 356 YETGRVIGDGNFAVVKECRHRETRQAYAMKIIDksrlkgkeDMVDSE 402

ikiLkk.dHPNIVkLydvfed.dklylVmEyceGdlGdLfdd1kkkrgrrg
i i ++ HPNIVkL++v+e++ ++yl++Ey+ G GdLf d + + +
69112 403 ILIIQSLSHPNIVKLHEVYETdMEIYLILEYVQG--GDLFDAIIESVK-- 448

1rkvlsE.earfyfrQilsaLeYLHsqqIiHRDLKPeNiLLds.....h
++E++a+ ++ ++++al ++H++ I+HRDLKPeN+L+ +++++++
69112 449 ----FPEpDAALMIMDLCKALVHMHDKSIVHRLDKPENLLVQRnedkstT 494

vKlaDFG1Arql....ttfvGTpeYmAPEvl...gYgkpavDiWS1Gc1l
+KlaDFG1A+++ ++ t++Gtp Y+APE+l+++gYg +vD+W+ G+il
69112 495 LKLADFGLAHVvrpiFTVCGTPTYVAPEILsekGYGL-EVDMWAAGVIL 543

yElltGkpPFp....qldlifkkig..... SpeakdLikk1
y+ll+G pPF++++++d++f++i ++ + ++++++ S+ akdL+++I
69112 544 YILLCGFPPFRsperDQDELNIIQlghfeflppywdniSDAAKDLVSRL 593

LvkdkPekRlta.eaLedaLdikaHPff<-*
Lv+dP+kR+ta++L+ HP++
69112 594 LVVDPKKRYTAhQVLQ-----HPWI 613

FIGURE 4B

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tyrkin_6: domain 1 of 1, from 356 to 613: score 50.0, E = 5.3e-15
*->ltlgkkLGeGaFGeVykGtlk...ieVAVktLkeda...keeFlrE
+ g+++G G+F +V +++ +++++ A K + ++ +++++ + +E
69112 356 YETGRVIGDGNFAVVKECRHRetrQAYAMKIIDKSRLkgkEDMVDSE 402

akiMkkLGgkHpNiVkkLlGvcteegrrFmevePlmivmEymegGdLldyL
+ i +l +HpNiVkL+ v ++ ++++++Ey+ gGdL d +
69112 403 ILIIQSL--SHPNIVKLHEVYETD-----MEIYLILEYVQGGDLFDAI 443

rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
++ + ++ +d + + +k + ++k +vHRDL N Lv +n +++
69112 444 IESVK-FPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLVQRNEdks 492

.vvKIsDFGLsRdlyddDkkGeskdyYrkkggkggktllPirWmAPEs1k
++ K +DFGL++ + + + +g APE 1
69112 493 tTLKLADFGLAKHVVRP-----IFTV---CGTP---TYVAPEILS 526

dgkFtskSDVWSFGV1LWEift1GeqPYpgeiqqfmsneevleylkkGyR
++ + + D W+ GV L+ i+ G +P ++ + +e+++ ++ G+
69112 527 EKGYGLEVDMWAAGVILY-ILLCGFPPFRSPE---RDQDEFNIIQLGHF 572

lpkPendlpiSsvtCPdelYdlM1qCWaedPedRptFsel..ver1<-*
P++ +d+ d1 ++ dP++R t ++ ++ +
69112 573 EFLPPY-----WDNISDAAKDLVSRLVVDPKKRYTAHQV1qHPWI 613

FIGURE 4C